

SEQUENCE LISTING

<110> Todderud, C. Gordon
Finger, Joshua N.
Rillema, Jill

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<150> 60/269,366

<151> 2001-02-16

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<170> PatentIn Ver. 2.1

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 35 40 45

Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys Cys Phe Ser Pro
 50 55 60

Ser Gly His Ile Leu Ala Ser Cys Ser Thr Asp Gly Thr Thr Val Leu
 65 70 75 80

Trp Asn Thr Glu Asn Gly Gln Met Leu Ala Val Met Glu Gln Pro Ser
 85 90 95

Gly Ser Pro Val Arg Val Cys Gln Phe Ser Pro Asp Ser Thr Cys Leu
 100 105 110

Ala Ser Gly Ala Ala Asp Gly Thr Val Val Leu Trp Asn Ala Gln Ser
 115 120 125

Tyr Lys Leu Tyr Arg Cys Gly Ser Val Lys Asp Gly Ser Leu Ala Ala
 130 135 140

Cys Ala Phe Ser Pro Asn Gly Ser Phe Phe Val Thr Gly Ser Ser Cys

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Lys Ala His Asp Leu Gly Ile Thr Cys Cys Asp Phe Ser Ser Gln Pro			
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Val Ser Asp Gly Glu Gln Gly Leu Gln Phe Phe Arg Leu Ala Ser Cys			
195	200	205	
Gly Gln Asp Cys Gln Val Lys Ile Trp Ile Val Ser Phe Thr His Ile			
210	215	220	
Leu Gly Phe Glu Leu Lys Tyr Lys Ser Thr Leu Ser Gly His Cys Ala			
225	230	235	240
Pro Val Leu Ala Cys Ala Phe Ser His Asp Gly Gln Met Leu Val Ser			
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Ile Leu His Thr Leu Thr Gln His Thr Arg Tyr Val Thr Thr Cys Ala			
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Phe Ala Pro Asn Thr Leu Leu Leu Ala Thr Gly Ser Met Asp Lys Thr			
290	295	300	
Val Asn Ile Trp Gln Phe Asp Leu Glu Thr Leu Cys Gln Ala Arg Arg			
305	310	315	320
Thr Glu His Gln Leu Lys Gln Phe Thr Glu Asp Trp Ser Glu Glu Asp			
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Val Ser Thr Trp Leu Cys Ala Gln Asp Leu Lys Asp Leu Val Gly Ile			
340	345	350	
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Glu Ser Leu Ala Asp Asp Leu Lys Ile Glu Ser Leu Gly Leu Arg Ser			
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Lys Val Leu Arg Lys Ile Glu Glu Leu Arg Thr Lys Val Lys Ser Leu			
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Ser Ser Gly Ile Pro Asp Glu Phe Ile Cys Pro Ile Thr Arg Glu Leu			

405

410

415

Met Lys Asp Pro Val Ile Ala Ser Asp Gly Tyr Ser Tyr Glu Lys Glu
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Ala Met Glu Asn Trp Ile Ser Lys Lys Lys Arg Thr Ser Pro Met Thr
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<213> HUMAN

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Cys	Phe	Ser	Pro	Ser	Gly	His	Ile	Leu	Ala	Ser	Cys	Ser	Thr	Asp	Gly
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 Phe Thr His Ile Leu Gly Phe Glu Leu Lys Tyr Lys Ser Thr Leu Ser
 260 265 270
 Gly His Cys Ala Pro Val Leu Ala Cys Ala Phe Ser Arg Asp Gly Gln
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 Met Leu Val Ser Gly Ser Val Asp Lys Ser Val Ile Val Tyr Asp Thr
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 Asn Thr Glu Asn Ile Leu His Thr Leu Thr Gln His Thr Arg Tyr Val
 305 310 315 320
 Thr Thr Cys Ala Phe Ala Pro Asn Thr Leu Leu Leu Ala Thr Gly Ser
 325 330 335
 Met Asp Lys Thr Val Asn Ile Trp Gln Phe Asp Leu Glu Thr Leu Cys
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 Gln Ala Arg Arg Thr Glu His Gln Leu Lys Gln Phe Thr Glu Asp Trp
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 Gly Leu Arg Ser Lys Val Leu Arg Lys Ile Glu Glu Leu Arg Thr Lys
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 Val Lys Ser Leu Ser Ser Gly Ile Pro Asp Glu Phe Ile Cys Pro Ile
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 Thr Arg Glu Leu Met Lys Asp Pro Val Ile Ala Ser Asp Gly Tyr Ser
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 Tyr Glu Lys Glu Ala Met Glu Asn Trp Ile Ser Lys Lys Lys Arg Thr
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1007140200

Ser Pro Met Thr Asn Leu Val Leu Pro Ser Ala Val Leu Thr Pro Asn
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Arg Thr Leu Lys Met Ala Ile Asn Arg Trp Leu Glu Thr His Gln Lys
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<213> HUMAN

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<223> 630 bp partial nucleic acid sequence of human
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<213> MOUSE

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<213> MOUSE

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Thr Ile Arg Leu Tyr Ser Leu Ser Asp Phe Val Glu Leu Pro Tyr Ser
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Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys Cys Phe Ser Pro
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Ser Gly His Val Leu Ala Ser Cys Ser Thr Asp Gly Thr Thr Val Leu
    65             70             75             80

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Trp Ser Ser His Ser Gly His Thr Leu Thr Val Leu Glu Gln Pro Gly

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1905

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<210> 9
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<213> RAT
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Ile His Lys Lys Lys Arg Thr Ser Pro Met Thr Asn Leu Ala Leu Pro
35 40 45

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<213> Podospora anserina

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<223> beta transducin-like protein encoded by the
het-e-1 gene

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20 25 30

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35 40 45

Arg Ala Val Ser Lys Leu Gly Tyr Asn Lys Ile Arg Phe Cys Ala Asp
50 55 60

Gln Ala Trp Arg Asp Gly Arg Lys Phe Phe Trp Val Asp Thr Cys Cys
65 70 75 80

Ile Asp Lys Ser Asn Ser Thr Glu Leu Gln Glu Ala Ile Asn Ser Met
85 90 95

Phe Arg Trp Tyr Arg Asp Ala Ala Lys Cys Tyr Val Tyr Leu Thr Asp
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Val Ser Thr Asp Lys Arg Asp Ala Asp Gly Asp Pro Ser Trp Lys Trp
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Ala Phe Gln Lys Cys Lys Trp Phe Thr Arg Gly Trp Thr Leu Gln Glu
 130 135 140

Leu Ile Ala Pro Thr Ser Val Glu Phe Phe Ser Arg Glu Lys Ala Arg
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Ile Gly Asp Arg Asn Ser Leu Glu Arg Met Ile His Asp Val Thr Gly
 165 170 175

Ile Pro Leu Glu Ala Leu Arg Gly Ser Pro Leu Ser Asp Phe Ser Val
 180 185 190

His Asp Arg Met Ala Trp Met Lys Gln Arg Asn Thr Thr Arg Glu Glu
 195 200 205

Asp Met Ala Tyr Ser Leu Phe Gly Ile Phe Asp Val His Leu Pro Leu
 210 215 220

Ile Tyr Gly Glu Gly Lys Glu Lys Ala Leu Glu Arg Leu Arg Glu Lys
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Ile Gly Lys Asp Asp Gly Cys Leu Ala Asp Leu Arg Val Thr Asp Pro
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 260 265 270

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 275 280 285

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Gly Lys Thr Met Leu Leu Cys Gly Ile Ile Asp Glu Leu Lys Lys Ser
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Thr Pro Pro Gly Leu Leu Ser Phe Phe Phe Cys Gln Ala Thr Asp Ser
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Val Ser Gln Gln Pro Ala Leu Ile Ser His Val Arg Arg Pro Tyr Asp
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1007744-001500

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Tyr Leu Ile Ile Asp Ala Leu Asp Glu Cys Val Thr Asp Leu Pro Gln
 405 410 415

Leu Leu Glu Leu Ile Thr Arg Thr Ser Cys Thr Ser Ser Pro Ile Lys
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Thr Ala Thr Gln Lys Ala Arg Leu Ser Leu Glu Leu Asn Ala Glu Ser
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Ile Ser Thr Ala Val Asn Ala Phe Ile Gln Asn Arg Ile Asp Gln Leu
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Ala Pro Lys Thr Lys His Asp Ala Asn Met Ile Gly Lys Ile Arg Asp
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 Gln Asp Asp Gly Asp Ile His Arg Phe Leu Thr Thr Lys Tyr Leu Tyr
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Arg Val Ala Ser Gly Ser Asp Asp Lys Thr Ile Lys Ile Trp Asp Ala
900 905 910

Ala Ser Gly Thr Cys Thr Gln Thr Leu Glu Gly His Gly Gly Arg Val
915 920 925

Gln Ser Val Ala Phe Ser Pro Asp Gly Gln Arg Val Ala Ser Gly Ser
930 935 940

Asp Asp His Thr Ile Lys Ile Trp Asp Ala Ala Ser Gly Thr Cys Thr
945 950 955 960

Gln Thr Leu Glu Gly His Gly Ser Ser Val Leu Ser Val Ala Phe Ser
965 970 975

Pro Asp Gly Gln Arg Val Ala Ser Gly Ser Gly Asp Lys Thr Ile Lys
980 985 990

Ile Trp Asp Thr Ala Ser Gly Thr Cys Thr Gln Thr Leu Glu Gly His
995 1000 1005

Gly Gly Ser Val Trp Ser Val Ala Phe Ser Pro Asp Gly Gln Arg Val
1010 1015 1020

Ala Ser Gly Ser Asp Asp Lys Thr Ile Lys Ile Trp Asp Thr Ala Ser
1025 1030 1035 1040

Gly Thr Cys Thr Gln Thr Leu Glu Gly His Gly Gly Trp Val Gln Ser
1045 1050 1055

Val Val Phe Ser Pro Asp Gly Gln Arg Val Ala Ser Gly Ser Asp Asp
1060 1065 1070

His Thr Ile Lys Ile Trp Asp Ala Val Ser Gly Thr Cys Thr Gln Thr
1075 1080 1085

Leu Glu Gly His Gly Asp Ser Val Trp Ser Val Ala Phe Ser Pro Asp
1090 1095 1100

Gly Gln Arg Val Ala Ser Gly Ser Ile Asp Gly Thr Ile Lys Ile Trp
1105 1110 1115 1120

Asp Ala Ala Ser Gly Thr Cys Thr Gln Thr Leu Glu Gly His Gly Gly
1125 1130 1135

Trp Val His Ser Val Ala Phe Ser Pro Asp Gly Gln Arg Val Ala Ser
1140 1145 1150

Gly Ser Ile Asp Gly Thr Ile Lys Ile Trp Asp Ala Ala Ser Gly Thr
1155 1160 1165

Cys Thr Gln Thr Leu Glu Gly His Gly Gly Trp Val Gln Ser Val Ala
1170 1175 1180

Phe Ser Pro Asp Gly Gln Arg Val Ala Ser Gly Ser Ser Asp Lys Thr
1185 1190 1195 1200

Ile Lys Ile Trp Asp Thr Ala Ser Gly Thr Cys Thr Gln Thr Leu Glu
1205 1210 1215

Gly His Gly Gly Trp Val Gln Ser Val Ala Phe Ser Pro Asp Gly Gln
1220 1225 1230

Arg Val Ala Ser Gly Ser Ser Asp Asn Thr Ile Lys Ile Trp Asp Thr
1235 1240 1245

Ala Ser Gly Thr Cys Thr Gln Thr Leu Asn Val Gly Ser Thr Ala Thr
1250 1255 1260

Cys Leu Ser Phe Asp Tyr Thr Asn Ala Tyr Ile Asn Thr Asn Ile Gly
1265 1270 1275 1280

Arg Ile Gln Ile Ala Thr Ala Thr Met Glu Ser Leu Asn Gln Leu Ser
1285 1290 1295

Ser Pro Val Cys Tyr Ser Tyr Gly Leu Gly Gln Asp His Arg Trp Ile
1300 1305 1310

Thr Cys Asn Asn Gln Asn Val Leu Trp Leu Pro Pro Glu Tyr His Thr
1315 1320 1325

Ser Ala Phe Thr Met Gln Gly Arg Lys Ile Val Leu Gly Ser Tyr Ser
1330 1335 1340

Gly Arg Ile Ile Ile Phe Leu Phe Ser Arg Asp Val
1345 1350 1355

<210> 11

<211> 742

<212> PRT

<213> Thermomonospora curvata

<220>

<223> amino acid sequence encoded by the PKWA gene

<400> 11

Met Ile Glu Pro Leu Gln Pro Gly Asp Pro Gly Arg Ile Gly Pro Tyr

1

5

10

15

Arg Leu Val Ser Arg Leu Gly Ala Gly Gly Met Gly Gln Val Phe Leu

20

25

30

Ala Arg Ser Pro Gly Gly Arg Pro Val Val Val Lys Val Ile Leu Pro

35

40

45

Glu Tyr Ala Asn Asp Asp Glu Tyr Arg Ile Arg Phe Ala Arg Glu Val

50

55

60

Glu Ala Ala Arg Arg Val Gly Gly Phe His Thr Ala Gln Val Ile Asp

65

70

75

80

Ala Asp Pro Thr Ala Asp Pro Pro Trp Met Ala Thr Ala Tyr Ile Pro

85

90

95

Gly Pro Ser Leu Arg Lys Ala Val Thr Glu Arg Gly Pro Leu Tyr Gly

100

105

110

Asn Asn Leu Arg Thr Leu Ala Ala Gly Leu Val Glu Gly Leu Ala Ala

115

120

125

Ile His Ala Cys Gly Leu Val His Arg Asp Phe Lys Pro Ser Asn Ile

130

135

140

Val Leu Ala Ala Asp Gly Pro Arg Val Ile Asp Phe Gly Val Ala Arg

145

150

155

160

Pro Leu Asp Ser Ser Val Met Thr Gln Ser Gly Ala Val Ile Gly Thr

165

170

175

Leu Ala Tyr Met Ser Pro Glu Gln Thr Asp Gly Ser Gln Val Gly Pro

180

185

190

Ala Ser Asp Val Phe Ser Leu Gly Thr Val Leu Ala Phe Ala Ala Thr

195

200

205

Gly Arg Ser Pro Phe Met Ala Asp Ser Ile Gly Glu Ile Ile Ala Arg

210

215

220

Ile Ser Gly Pro Pro Pro Glu Leu Pro Glu Leu Pro Asp Asp Leu Arg

10077411021500

225		230		235		240									
Glu	Leu	Val	Tyr	Ala	Cys	Trp	Glu	Gln	Asn	Pro	Asp	Leu	Arg	Pro	Thr
				245					250					255	
Thr	Ala	Glu	Leu	Leu	Ala	Gln	Leu	Ser	Thr	Asp	His	Thr	Gly	Asp	Asp
			260					265					270		
Trp	Pro	Pro	Pro	His	Leu	Ser	Asp	Leu	Ile	Gly	Ser	Met	Leu	Pro	Leu
		275					280					285			
Gly	Ala	Thr	Thr	Ser	Pro	Asn	Pro	Ser	Leu	Ala	Ile	Glu	Pro	Pro	Pro
	290					295					300				
Pro	Ser	His	Gly	Pro	Pro	Arg	Pro	Ser	Glu	Pro	Leu	Pro	Asp	Pro	Gly
305					310				315					320	
Asp	Asp	Ala	Asp	Glu	Pro	Ser	Ala	Glu	Lys	Pro	Ser	Arg	Thr	Leu	Pro
				325				330						335	
Glu	Pro	Glu	Pro	Pro	Glu	Leu	Glu	Glu	Lys	Pro	Ile	Gln	Val	Ile	His
			340					345					350		
Glu	Pro	Glu	Arg	Pro	Ala	Pro	Thr	Pro	Pro	Arg	Pro	Arg	Glu	Pro	Ala
		355					360					365			
Arg	Gly	Ala	Ile	Lys	Pro	Lys	Asn	Pro	Arg	Pro	Ala	Ala	Pro	Gln	Pro
	370					375					380				
Pro	Trp	Ser	Pro	Pro	Arg	Val	Gln	Pro	Pro	Arg	Trp	Lys	Gln	Leu	Ile
385					390				395					400	
Thr	Lys	Lys	Pro	Val	Ala	Gly	Ile	Leu	Thr	Ala	Val	Ala	Thr	Ala	Gly
			405					410					415		
Leu	Val	Val	Ser	Phe	Leu	Val	Trp	Gln	Trp	Thr	Leu	Pro	Glu	Thr	Pro
			420					425					430		
Leu	Arg	Pro	Asp	Ser	Ser	Thr	Ala	Pro	Ser	Glu	Ser	Ala	Asp	Pro	His
		435					440					445			
Glu	Leu	Asn	Glu	Pro	Arg	Ile	Leu	Thr	Thr	Asp	Arg	Glu	Ala	Val	Ala
	450					455					460				
Val	Ala	Phe	Ser	Pro	Gly	Gly	Ser	Leu	Leu	Ala	Gly	Gly	Ser	Gly	Asp
465					470					475				480	
Lys	Leu	Ile	His	Val	Trp	Asp	Val	Ala	Ser	Gly	Asp	Glu	Leu	His	Thr

485	490	495
Leu Glu Gly His Thr Asp Trp Val Arg Ala Val Ala Phe Ser Pro Asp		
500	505	510
Gly Ala Leu Leu Ala Ser Gly Ser Asp Asp Ala Thr Val Arg Leu Trp		
515	520	525
Asp Val Ala Ala Ala Glu Glu Arg Ala Val Phe Glu Gly His Thr His		
530	535	540
Tyr Val Leu Asp Ile Ala Phe Ser Pro Asp Gly Ser Met Val Ala Ser		
545	550	555
Gly Ser Arg Asp Gly Thr Ala Arg Leu Trp Asn Val Ala Thr Gly Thr		
565	570	575
Glu His Ala Val Leu Lys Gly His Thr Asp Tyr Val Tyr Ala Val Ala		
580	585	590
Phe Ser Pro Asp Gly Ser Met Val Ala Ser Gly Ser Arg Asp Gly Thr		
595	600	605
Ile Arg Leu Trp Asp Val Ala Thr Gly Lys Glu Arg Asp Val Leu Gln		
610	615	620
Ala Pro Ala Glu Asn Val Val Ser Leu Ala Phe Ser Pro Asp Gly Ser		
625	630	635
Met Leu Val His Gly Ser Asp Ser Thr Val His Leu Trp Asp Val Ala		
645	650	655
Ser Gly Glu Ala Leu His Thr Phe Glu Gly His Thr Asp Trp Val Arg		
660	665	670
Ala Val Ala Phe Ser Pro Asp Gly Ala Leu Leu Ala Ser Gly Ser Asp		
675	680	685
Asp Arg Thr Ile Arg Leu Trp Asp Val Ala Ala Gln Glu Glu His Thr		
690	695	700
Thr Leu Glu Gly His Thr Glu Pro Val His Ser Val Ala Phe His Pro		
705	710	715
Glu Gly Thr Thr Leu Ala Ser Ala Ser Glu Asp Gly Thr Ile Arg Ile		
725	730	735
Trp Pro Ile Ala Thr Glu		

<210> 12
 <211> 1272
 <212> DNA
 <213> HUMAN

<220>
 <223> RET 16.2 splice variant

<400> 12
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 gatcccgcgc gcccccgctc ctgcaggctg tttttcttca aataaagaac atggtgaaac 120
 tgattcacac attagctgat catggtgacg atgtcaactg ctgtgccttc tccttttccc 180
 tcttggttac ttgctccttg gacaaaacaa ttgcgcctgta ctcgttacgt gactttactg 240
 aactgccaca ttctccattg aagtttcata cctatgctgt ccactgctgc tgtttctccc 300
 cttcaggaca tattttggca tcgtgttcaa cagatggtac cactgtccta tggaatactg 360
 aaaatggaca gatgctggca gtgatggaac agcctagtgg cagccctgtg agggtttgcc 420
 agttttcccc agactccacg tgtttggcat caggggcagc tgatggaact gtgggtttgt 480
 ggaatgcaca gtcatacaaa ttatatagat gtggtagtgt taaagatggc tccttggcgg 540
 catgtgcatt ttctcctaag ggaagcttct ttgtcactgg ctctcatgt ggtgatttaa 600
 cagtgtggga tgataaaatg aggtgtctgc atagtgaaaa agcacatgat cttggaatta 660
 cctgctgcga tttttcttca cagccagttt ctgatggaga acaaggctct cagttttttc 720
 gactggcatc atgtggctcag gattgccaag tcaaaatttg gattgtttct tttaccata 780
 tcttagcaag gcgcacagaa catcagctga agcaatttac cgaagattgg tcagaggagg 840
 tcgtctcaac atggctttgt gcacaagatt taaaagatct tgttgggtatt ttcaagatga 900
 ataacattga tggaaaagaa ctgttgaatc ttacaaaaga aagtctggct gatgatttga 960
 aaattgaatc tctaggactg cgtagttaaag tgctgaggaa aattgaagag ctacaggacca 1020
 aggttaaadc cttttcttca ggaattcctg atgaatttat atgtccaata actagagaac 1080
 ttatgaaaga tccggtcatc gcatcagatg gctattcata tgaaaaggaa gcaatggaaa 1140
 attggatcag caaaaagaaa cgtacaagtc ccatgacaaa tcttgttctt ctttcagcgg 1200
 tacttacacc aaataggact ctgaaaatgg ccatcaatag atggctggag acacacccaaa 1260
 agtaaagaat tc 1272

<210> 13
 <211> 384
 <212> PRT
 <213> HUMAN

<220>
 <223> RET 16.2 splice variant

<400> 13
 Met Val Lys Leu Ile His Thr Leu Ala Asp His Gly Asp Asp Val Asn
 1 5 10 15

Cys Cys Ala Phe Ser Phe Ser Leu Leu Ala Thr Cys Ser Leu Asp Lys
 20 25 30

Thr Ile Arg Leu Tyr Ser Leu Arg Asp Phe Thr Glu Leu Pro His Ser
 35 40 45

Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys Cys Phe Ser Pro
 50 55 60

Ser Gly His Ile Leu Ala Ser Cys Ser Thr Asp Gly Thr Thr Val Leu
 65 70 75 80

Trp Asn Thr Glu Asn Gly Gln Met Leu Ala Val Met Glu Gln Pro Ser
 85 90 95

Gly Ser Pro Val Arg Val Cys Gln Phe Ser Pro Asp Ser Thr Cys Leu
 100 105 110

Ala Ser Gly Ala Ala Asp Gly Thr Val Val Leu Trp Asn Ala Gln Ser
 115 120 125

Tyr Lys Leu Tyr Arg Cys Gly Ser Val Lys Asp Gly Ser Leu Ala Ala
 130 135 140

Cys Ala Phe Ser Pro Asn Gly Ser Phe Phe Val Thr Gly Ser Ser Cys
 145 150 155 160

Gly Asp Leu Thr Val Trp Asp Asp Lys Met Arg Cys Leu His Ser Glu
 165 170 175

Lys Ala His Asp Leu Gly Ile Thr Cys Cys Asp Phe Ser Ser Gln Pro
 180 185 190

Val Ser Asp Gly Glu Gln Gly Leu Gln Phe Phe Arg Leu Ala Ser Cys
 195 200 205

Gly Gln Asp Cys Gln Val Lys Ile Trp Ile Val Ser Phe Thr His Ile
 210 215 220

Leu Ala Arg Arg Thr Glu His Gln Leu Lys Gln Phe Thr Glu Asp Trp
 225 230 235 240

Ser Glu Glu Val Val Ser Thr Trp Leu Cys Ala Gln Asp Leu Lys Asp
 245 250 255

Leu Val Gly Ile Phe Lys Met Asn Asn Ile Asp Gly Lys Glu Leu Leu
 260 265 270

2025-11-02 14:00:21

Asn Leu Thr Lys Glu Ser Leu Ala Asp Asp Leu Lys Ile Glu Ser Leu
 275 280 285

Gly Leu Arg Ser Lys Val Leu Arg Lys Ile Glu Glu Leu Arg Thr Lys
 290 295 300

Val Lys Ser Leu Ser Ser Gly Ile Pro Asp Glu Phe Ile Cys Pro Ile
 305 310 315 320

Thr Arg Glu Leu Met Lys Asp Pro Val Ile Ala Ser Asp Gly Tyr Ser
 325 330 335

Tyr Glu Lys Glu Ala Met Glu Asn Trp Ile Ser Lys Lys Lys Arg Thr
 340 345 350

Ser Pro Met Thr Asn Leu Val Leu Pro Ser Ala Val Leu Thr Pro Asn
 355 360 365

Arg Thr Leu Lys Met Ala Ile Asn Arg Trp Leu Glu Thr His Gln Lys
 370 375 380

<210> 14

<211> 1908

<212> DNA

<213> HUMAN

<220>

<223> RET 16.3 splice variant

<400> 14

gaattcggct cgaggccggc gcccgccccg ccagcctcac ctgcgcgga cgtgacccgc 60
 accgcccgtg ggcacctga aggcggatcc cgcgcgcccc cgctcctgca ggctgttttt 120
 cttcaaataa agaacatggg gaaactgatt cacacattag ctgatcatgg tgacgatgtc 180
 aactgctgtg ctttctcctt ttccctcttg gctacttgct ctttgacaa aacaattcgc 240
 ctgtactcgt tacgtgactt tactgaactg ccacattctc cattgaagtt tcatacctat 300
 gctgtccact gctgctgttt ctccccttca ggacatattt tggcatcgtg ttcaacagat 360
 ggtaccactg tcctatggaa tactgaaaat ggacagatgc tggcagtgat ggaacagcct 420
 agtggcagcc ctgtgagggt ttgccagttt tcccagact ccacgtgttt ggcacaggg 480
 gcagctgatg gaactgtggg tttgtggaat gcacagtcac acaaattata tagatgtggg 540
 agtggttaaag atggctcctt ggcggcatgt gcattttctc ctaatggaag cttctttgtc 600
 actggctcct catgtggtga tttaacagtg tgggatgata aaatgagggt tctgcatagt 660
 gaaaaagcac atgatcttgg aattacctgc tgcgattttt cttcacagcc agtttctgat 720
 ggagaacaag gtcttcagtt ttttcgactg gcatcatgtg gtcaggattg ccaagtcaaa 780
 atttggattg tttcttttac ccatacttta ggttttgaat taaaatataa aagtacactg 840

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agtgggcact gtgctcctgt tctggccttgt gctttttccc atgatgggca gatgctagtc 900
tcagggtcag tggataagtc tgtcatagta tatgatacta atactgagaa tatacttcac 960
acattgactc agcacaccag gtatgtcaca acttgtgctt ttgcaccta taccctttta 1020
cttgctactg gttcaatgga caaacacgtg aacatctggc aatttgacct ggaaacactt 1080
tgccaagcaa ggcgcacaga acatcagctg aagcaattta ccgaagattg gtcagaggag 1140
gatgtctcaa catggccttg tgcacaagat ttaaaagatc ttgttggtat tttcaagatg 1200
aataacattg atggaaaaga actgttgaat cttacaaaag aaagtctggc tgatgatttg 1260
aaaattggct ggagtcctct ggcatggcca tgcctcactg cagcttcaac ctctggggct 1320
caagtgatcc tcctacctcg gcctcaatct ctaggactgc gtagtaaagt gctgaggaaa 1380
attgaagagc tcaggaccaa gggttaaacc ctttcttcag gaattcctga tgaatttata 1440
tgtccaataa ctagagaact tatgaaagat cgggtcatcg catcagatgg ctattcatat 1500
gaaaaggaag caatggaaaa ttggatcagc aaaaagaaac gtacaagtcc catgacaaat 1560
cttgttcttc cttcagcggc acttacacca aataggactc tgaaaatggc catcaataga 1620
tggctggaga cacaccaaaa gtaaaattgt tgatattgta ttatttatat tttcagtgat 1680
ctcatttgaa tgatttatag gtaataacta atcagacatt attaaaagca aaacaggaaa 1740
aaggtaaact tcttaaattt agttacatat aaaaattgtc aattttcatt ctttaaaaaa 1800
cacatggact tactataaaa gcctttttgt actagtgaag agaatcttca gctatataga 1860
aataaaagta tccttttaaaa aaaaaaaaaa aaaaaaaagg gcggccgc 1908

<210> 15

<211> 502

<212> PRT

<213> HUMAN

<220>

<223> RET 16.3 splice variant

<400> 15

Met Val Lys Leu Ile His Thr Leu Ala Asp His Gly Asp Asp Val Asn

1 5 10 15

Cys Cys Ala Phe Ser Phe Ser Leu Leu Ala Thr Cys Ser Leu Asp Lys

20 25 30

Thr Ile Arg Leu Tyr Ser Leu Arg Asp Phe Thr Glu Leu Pro His Ser

35 40 45

Pro Leu Lys Phe His Thr Tyr Ala Val His Cys Cys Cys Phe Ser Pro

50 55 60

Ser Gly His Ile Leu Ala Ser Cys Ser Thr Asp Gly Thr Thr Val Leu

65 70 75 80

Trp Asn Thr Glu Asn Gly Gln Met Leu Ala Val Met Glu Gln Pro Ser

85 90 95

Gly Ser Pro Val Arg Val Cys Gln Phe Ser Pro Asp Ser Thr Cys Leu

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100	105	110
Ala Ser Gly Ala Ala Asp Gly Thr Val Val Leu Trp Asn Ala Gln Ser		
115	120	125
Tyr Lys Leu Tyr Arg Cys Gly Ser Val Lys Asp Gly Ser Leu Ala Ala		
130	135	140
Cys Ala Phe Ser Pro Asn Gly Ser Phe Phe Val Thr Gly Ser Ser Cys		
145	150	155
Gly Asp Leu Thr Val Trp Asp Asp Lys Met Arg Cys Leu His Ser Glu		
165	170	175
Lys Ala His Asp Leu Gly Ile Thr Cys Cys Asp Phe Ser Ser Gln Pro		
180	185	190
Val Ser Asp Gly Glu Gln Gly Leu Gln Phe Phe Arg Leu Ala Ser Cys		
195	200	205
Gly Gln Asp Cys Gln Val Lys Ile Trp Ile Val Ser Phe Thr His Ile		
210	215	220
Leu Gly Phe Glu Leu Lys Tyr Lys Ser Thr Leu Ser Gly His Cys Ala		
225	230	235
Pro Val Leu Ala Cys Ala Phe Ser His Asp Gly Gln Met Leu Val Ser		
245	250	255
Gly Ser Val Asp Lys Ser Val Ile Val Tyr Asp Thr Asn Thr Glu Asn		
260	265	270
Ile Leu His Thr Leu Thr Gln His Thr Arg Tyr Val Thr Thr Cys Ala		
275	280	285
Phe Ala Pro Asn Thr Leu Leu Leu Ala Thr Gly Ser Met Asp Lys Thr		
290	295	300
Val Asn Ile Trp Gln Phe Asp Leu Glu Thr Leu Cys Gln Ala Arg Arg		
305	310	315
Thr Glu His Gln Leu Lys Gln Phe Thr Glu Asp Trp Ser Glu Glu Asp		
325	330	335
Val Ser Thr Trp Leu Cys Ala Gln Asp Leu Lys Asp Leu Val Gly Ile		
340	345	350
Phe Lys Met Asn Asn Ile Asp Gly Lys Glu Leu Leu Asn Leu Thr Lys		

355 360 365
 Glu Ser Leu Ala Asp Asp Leu Lys Ile Gly Trp Ser Pro Leu Ala Trp
 370 375 380

 Ser Cys Leu Thr Ala Ala Ser Thr Ser Trp Ala Gln Val Ile Leu Leu
 385 390 395 400

 Pro Arg Pro Gln Ser Leu Gly Leu Arg Ser Lys Val Leu Arg Lys Ile
 405 410 415

 Glu Glu Leu Arg Thr Lys Val Lys Ser Leu Ser Ser Gly Ile Pro Asp
 420 425 430

 Glu Phe Ile Cys Pro Ile Thr Arg Glu Leu Met Lys Asp Pro Val Ile
 435 440 445

 Ala Ser Asp Gly Tyr Ser Tyr Glu Lys Glu Ala Met Glu Asn Trp Ile
 450 455 460

 Ser Lys Lys Lys Arg Thr Ser Pro Met Thr Asn Leu Val Leu Pro Ser
 465 470 475 480

 Ala Val Leu Thr Pro Asn Arg Thr Leu Lys Met Ala Ile Asn Arg Trp
 485 490 495

 Leu Glu Thr His Gln Lys
 500

<210> 16
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 11587
 oligonucleotide

<400> 16
 gcacagccgc caaggagcca c

21

<210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer, JNF
346

<400> 17

tcacctgctgac ggcacgtgac cc

22

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer, JNF
493

<400> 18

tttacttttg gtgtgtctcc agcc

24

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer, JNF
494

<400> 19

ttacttttgg tgtgtctcca gccatctatt gatggc

36

<210> 20

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer, JNF
232

<400> 20

ggcagatgct agtctcaggg

20

<210> 21

<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer, JNF
233

<400> 21

gggatttaac cttggtcctg

20

<210> 22

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide, 11590

<400> 22

gcacacacgc agccagaga

19

<210> 23

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide, 11591

<400> 23

agagaccgac gcacacacg

19

<210> 24

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: U box domain
of RET16

<400> 24

Glu Phe Ile Cys Pro Ile Thr Arg Glu Leu Met Lys Asp Pro Val Ile
1 5 10 15

Ala Ser Asp Gly Tyr Ser Tyr Glu Lys Glu Ala Met Glu Asn Trp Ile
20 25 30

Ser Lys Lys Lys Arg Thr Ser Pro Met Thr Asn Leu Val Leu Pro Ser
35 40 45

Ala Val
50

<210> 25

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: U box domain
of PRP19

<400> 25

Met Leu Cys Ala Ile Ser Gly Lys Val Pro Arg Arg Pro Val Leu Ser
1 5 10 15

Pro Lys Ser Arg Thr Ile Phe Glu Lys Ser Leu Leu Glu Gln Tyr Val
20 25 30

Lys Asp Thr Gly Asn Asp Pro Ile Thr Asn Glu Pro Leu Ser Ile Glu
35 40 45

Glu Ile Val Glu
50